

Tyr Ser Ser Ser Val Ile Phe Val Leu Thr Ile Gly Lys Gly Val Tyr

2/14

195                      200                      205  
 Ala Phe Thr Leu Asp Pro Met Tyr Gly Glu Phe Val Leu Thr Ser Glu  
 210                      225                      220  
 Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly  
 225                      230                      235                      240  
 Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu  
 245                      250                      255  
 Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly  
 260                      265                      270  
 Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr  
 275                      280                      285  
 Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu  
 290                      295                      300  
 Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys  
 305                      310                      315                      320  
 Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile  
 325                      330                      335  
 His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys  
 340                      345                      350  
 Leu Glu Lys Tyr Leu Ala  
 355

&lt;210&gt; 2

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Spinacia oleracea L

&lt;220&gt; Fructose-1,6-bisphosphatase

&lt;223&gt;

&lt;400&gt; 2

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 gctggatatt ctaacttgac tggattcaa ggtgctgtca atatccaagg agaggatcag 240  
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<210> 3

<211> 333

<212> PRT

<213> Spinacia oleracea L

<220> Sedoheptulose-1,7-bisphosphatase

<223>

<400> 3

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                   20                  25                  30  
 Ile Arg Leu Met Met Cys Met Gly Glu Ala Leu Arg Thr Ile Gly Phe  
                   35                  40                  45  
 Lys Val Arg Thr Ala Ser Cys Gly Gly Thr Gln Cys Val Asn Thr Phe  
                   50                  55                  60  
 Gly Asp Glu Gln Leu Ala Ile Asp Val Leu Ala Asp Lys Leu Leu Phe  
                   65                  70                  75                  80  
 Glu Ala Leu Asn Tyr Ser His Phe Cys Lys Tyr Ala Cys Ser Glu Glu  
                   85                  90                  95  
 Leu Pro Glu Leu Gln Asp Met Gly Gly Pro Val Asp Gly Gly Phe Ser  
                   100                  105                  110  
 Val Ala Phe Asp Pro Leu Asp Gly Ser Ser Ile Val Asp Thr Asn Phe  
                   115                  120                  125  
 Ser Val Gly Thr Ile Phe Gly Val Trp Pro Gly Asp Lys Leu Thr Gly  
                   130                  135                  140  
 Val Thr Gly Arg Asp Gln Val Ala Ala Ala Met Gly Ile Tyr Gly Pro  
                   145                  150                  155                  160  
 Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu  
                   165                  170                  175  
 Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr  
                   180                  185                  190  
 Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr  
                   195                  200                  205  
 Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu

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210	215	220
Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln		
225	230	235
Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr		
245	250	255
Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe		
260	265	270
Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val		
275	280	285
Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr		
290	295	300
Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser		
305	310	315
Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala		
325	330	

&lt;210&gt; 4

&lt;211&gt; 999

&lt;212&gt; DNA

&lt;213&gt; Spinacia oleracea L

&lt;220&gt; Sedoheptulose-1,7-bisphosphatase

&lt;223&gt;

&lt;400&gt; 4

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gagttcctag caaaggcaac cacagataaa gggctgatta gattgatgat gtgcatggga	120
gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggigg aactcaatgt	180
gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttcttttc	240
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caagatatgg gagggccgtg tgatggcgga ttcagigtat catttgaccc ccttgatgga	360
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caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc	960
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&lt;210&gt; 5

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&lt;211&gt; 356

&lt;212&gt; PRT

&lt;213&gt; Synechococcus

<220> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus  
PCC 7942

&lt;223&gt;

&lt;400&gt; 5

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Met Glu Lys Thr Ile Gly Leu Glu Ile Ile Glu Val Val Glu Gln Ala
      5              10              15
Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala
      20              25              30
Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu
      35              40              45
Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro
      50              55              60
Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys
      65              70              75              80
Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val
      85              90              95
Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser
      100             105             110
Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro
      115             120             125
Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys
      130             135             140
Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu
      145             150             155             160
Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg
      165             170             175
Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg
      180             185             190
Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly
      195             200             205
Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro
      210             215             220
Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe
      225             230             235             240
Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile
      245             250             255
Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile

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260 265 270  
 Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln  
 275 280 285  
 Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu  
 290 295 300  
 Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile  
 305 310 315 320  
 Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe  
 325 330 335  
 Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp  
 340 345 350  
 Arg Pro Glu Arg  
 355

&lt;210&gt; 6

&lt;211&gt; 1350

&lt;212&gt; DNA

&lt;213&gt; Synechococcus

<220> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus  
 PCC. 7942

&lt;400&gt; 6

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cgaaaagaat gaagccgatc gcgtcgagc agaagcgaig cgggtgcgga tgaaccaagt	240
ggaaatgctg gggcgcatcg tcatcggtga aggcgagcgc gacgaagcac cgatgctcia	300
tatcggtigaa gaagtgggca tctaccgga tgcagacaag cgggctggcg taccggctgg	360
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aaacggcctc atgcatctcg cagtgtcgg ctcagccatc ggacagcacc gg	1312

&lt;210&gt; 7

&lt;211&gt; 133

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; psbA promoter

&lt;400&gt; 7

agcttctaca tacaccttgg ttgacacgag tatataagtc atgttatact gttgaataac	60
aagccttcca ttttctattt tgattttag aaaactagtg tgcttgggag tccctgatga	120
ttaaataaac caa	133

&lt;210&gt; 8

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; rps16 terminator

&lt;400&gt; 8

agcttgaat tcaattaagg aaataaatta aggaaataca aaaagggggg tagtcatttg	60
tatataactt tgtatgactt ttctcttcta tttttttgta tttcctccct ttccttttct	120
atttgtattt ttttatcatt gcttccattg aattactag	159

&lt;210&gt; 9

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;223&gt; aadA

&lt;400&gt; 9

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gcgtcatcga gcgccatctc gaaccgacgt tgctggccgt acatttgtac ggctccgcag	120
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cccagtatca gcccgcatca cttgaagcta gacaggctta tcttggacaa gaagaagatc	720

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<213> Artificial sequence	
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attgaattac tagtcgacct cgaggggggg cccgggtacc aattcgccct atagttagtc	3960
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ctgtagcggc gcattaagcg cggcgggtgt ggtggttacg cgcagcgtga ccgctacact	4200
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cggctttccc cgtcaagctc taaatcgggg gctcccttta gggttccgat ttagtgcttt	4320

10/14

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&lt;210&gt; 11

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; multi-cloning regions

&lt;400&gt; 11

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&lt;210&gt; 12

&lt;211&gt; 142

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; rrn promoter

&lt;400&gt; 12

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 gacgtlagggg ggcagggatg gctatatttc tgggagcgaa ctccgggcga atttgaagcg 120  
 ctggataca gttgtaggga gg 142

&lt;210&gt; 13

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; psbA terminator

&lt;400&gt; 13

gatcctggcc tagtctatag gaggttttga aaagaaagga gcaataatca ttttcttggt 60  
 ctaicaagag ggtgctattg ctcttttctt tttttcttiti tatttattta ctagtatttt 120  
 acttacatag acttttttgt ttacattata gaaaaagaag gagaggttat tttcttgcatt 180  
 ttattcatga ttgagtattc tattttgatt ttgtatttgt ttaaaattgt agaaatagaa 240  
 cttgtttctc ttcttgctaa tgttactata tctttttgat ttttttttc caaaaaaaaa 300  
 tcaaattttg acttcttctt atctcttata tttgaataac tcttatctti gaaataataa 360  
 tatcatigaa ataagaaaga agagctatat 390

&lt;210&gt; 14

&lt;211&gt; 5581

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; pLD200

&lt;400&gt; 14

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accataigcg	gtagaaata	ccgcacagat	gcgtaaggag	aaaataccgc	atcaggcgcc	240
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gaaaccatta ttatcatgac attaacctat aaaaataggc gtatcacgag gcccttctgt	5580
c	5581

&lt;210&gt; 15

&lt;211&gt; 1434

&lt;212&gt; DNA

<213> *Nicotiana tabacum*

&lt;223&gt; rbcL

&lt;400&gt; 15

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aaattgactt attatactcc tgagtlacaa accaaggat actgatataat ggcagcattc	120
cgagtaactc ctcaacctgg agttccacct gaagaagcag gggccgcggt agctgccgaa	180
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cagttcgggtg gaggaacttt aggacaicct tggggtaatg cgccagggtgc cgtagctaata 1260  
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 ggtaaatgaaa ttattcgga ggcttgcaaa tggagccgg aactagctgc tgcttgtgaa 1380  
 gtaiggaag agatcgtatt taattttgca gcagtggaacg ttttgataa gtaa 1434

&lt;210&gt; 16

&lt;211&gt; 705

&lt;212&gt; DNA

<213> *Nicotiana tabacum*

&lt;223&gt; accD

&lt;400&gt; 16

aatgactatt catctattgt attttcatgc aaataggggg caagaaaact ctatggaaag 60  
 atgggtgggtt aattcgatgt tgtttaagaa ggagttcgaa cgcagggtgtg ggctaaataa 120  
 atcaatgggc agtcttggtc ctattgaaaa taccaatgaa gatccaaatc gaaaagttaa 180  
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 gaataatgga tttaggggcg aagatcccta ctataattct tacatgtatg atactcaata 480  
 tagttggaat aatcacatta atagttgcat tgaatgttat cttcagtcct aaatctgtat 540  
 agatacttcc attataagtg gtagtgagaa ttacggtgac agttacattt atagggccgt 600  
 ttgigggtgtt gaaagtcgaa atagtagtga aaacgagggt tccagtagac gaactcgcac 660  
 gaagggcagt gatttaacta taagagaaag ttctaataat ctcga 705

&lt;210&gt; 17

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; polylinker

&lt;400&gt; 17

cgcgccgcg ctagcgtcga c

21

&lt;210&gt; 18

&lt;211&gt; 7

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; Shine-Dalgarno Sequence

&lt;400&gt; 18

aggaggu

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